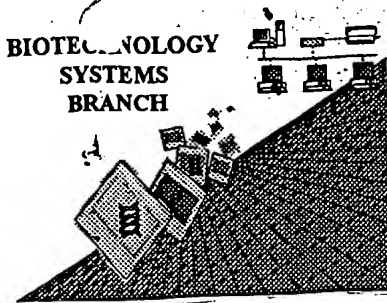


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



0400
0590
0118

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/993,420

Source: OIPE

Date Processed by STIC: 12/6/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 091993, 420

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

#2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/993,420

DATE: 12/06/2001
TIME: 15:19:49

Input Set : A:\01997.201006.SEQLIST.TXT
Output Set: N:\CRF3\12062001\I993420.raw

Does Not Comply
Corrected Diskette Needed

Errors on p 2

4 <110> APPLICANT: Horvitz, H. Robert
5 Hengartner, Michael
7 <120> TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
8 GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
9 USES THEREOF
11 <130> FILE REFERENCE: 01997/201006
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/993,420
C--> 13 <141> CURRENT FILING DATE: 2001-11-06
13 <150> PRIOR APPLICATION NUMBER: 09/234,186
14 <151> PRIOR FILING DATE: 1999-01-20
16 <150> PRIOR APPLICATION NUMBER: 07/898,933
17 <151> PRIOR FILING DATE: 1992-06-12
19 <150> PRIOR APPLICATION NUMBER: 07/927,681
20 <151> PRIOR FILING DATE: 1992-08-10
22 <150> PRIOR APPLICATION NUMBER: 08/288,295
23 <151> PRIOR FILING DATE: 1994-08-10
25 <150> PRIOR APPLICATION NUMBER: 08/801,248
26 <151> PRIOR FILING DATE: 1997-02-19
28 <160> NUMBER OF SEQ ID NOS: 8
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

245 <210> SEQ ID NO: 3
246 <211> LENGTH: 280
247 <212> TYPE: PRT
248 <213> ORGANISM: Caenorhabditis elegans
250 <400> SEQUENCE: 3
251 Met Thr Arg Cys Thr Ala Asp Asn Ser Leu Thr Asn Pro Ala Tyr Arg
252 1 5 10 15
253 Arg Arg Thr Met Ala Thr Gly Glu Met Lys Glu Phe Leu Gly Ile Lys
254 20 25 30
255 Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln Asp Leu
256 35 40 45
257 Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile Gly Glu
258 50 55 60
259 Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu Asp Ile
260 65 70 75 80
261 Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln Asn Gly
262 85 90 95
263 Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln Pro Glu
264 100 105 110
265 His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys His Ala
266 115 120 125
267 Glu Asn Phe Glu Thr Phe Cys Glu Gln Leu Leu Ala Val Pro Arg Ile
268 130 135 140

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/993,420

DATE: 12/06/2001
TIME: 15:19:50

Input Set : A:\01997.201006.SEQLIST.TXT
Output Set: N:\CRF3\12062001\I993420.raw

```

269 Ser Phe Ser Leu Tyr Gln Asp Val Val Arg Thr Val Gly Asn Ala Gln
270 145                               150                               155                               160
271 Thr Asp Gln Cys Pro Met Ser Tyr Gly Arg Leu Ile Gly Leu Ile Ser
272                               165                               170                               175
273 Phe Gly Gly Phe Val Ala Ala Lys Met Met Glu Ser Val Glu Leu Gln
274                               180                               185                               190
275 Gly Gln Val Arg Asn Leu Phe Val Tyr Thr Ser Leu Phe Ile Lys Thr
276                               195                               200                               205
277 Arg Ile Arg Asn Asn Trp Lys Glu His Asn Arg Ser Trp Asp Asp Phe
278                               210                               215                               220
279 Met Thr Leu Gly Lys Gln Met Lys Glu Asp Tyr Glu Arg Ala Glu Ala
280 225                               230                               235                               240
281 Glu Lys Val Gly Arg Arg Lys Gln Asn Arg Arg Trp Ser Met Ile Gly
282                               245                               250                               255

```

E--> 283

Ala Gly Val Thr Ala Gly Ala Ile Gly Ile Val Gly Val Val Val Cys

```

705 <210> SEQ ID NO: 8
706 <211> LENGTH: 239
707 <212> TYPE: PRT
708 <213> ORGANISM: Homo sapiens
710 <400> SEQUENCE: 8
711 Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
712 1                               5                               10                               15
713 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
714                               20                               25                               30
715 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
716                               35                               40                               45
717 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
718                               50                               55                               60
719 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
720 65                               70                               75                               80
721 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
722                               85                               90                               95
723 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
724                               100                              105                              110
725 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
726                               115                              120                              125
727 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
728                               130                              135                              140
729 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
730 145                              150                              155                              160
731 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
732                               165                              170                              175
733 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
734                               180                              185                              190
735 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
736                               195                              200                              205

```

E--> 737

Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala

210

215

misalignment

260

*misalignment
of amino acid
numbering*

*Please see error summary
sheet, item 3*

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/993,420

DATE: 12/06/2001

TIME: 15:19:51

Input Set : A:\01997.201006.SEQLIST.TXT
Output Set: N:\CRF3\12062001\I993420.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:283 M:252 E: No. of Seq. differs, <211>LENGTH:Input:280 Found:256 SEQ:3
L:737 M:252 E: No. of Seq. differs, <211>LENGTH:Input:239 Found:208 SEQ:8